

0200

OICE

#6

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/553,431

DATE: 05/04/2000

TIME: 16:30:29

Input Set : A:\Un900411.app

Output Set: N:\CRF3\05042000\I553431.raw

3 <110> APPLICANT: Osteryoung, Katherine W.  
 5 <120> TITLE OF INVENTION: Manipulation of Min Genes in Plants  
 7 <130> FILE REFERENCE: 920905.90041  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/553,431  
 C--> 10 <141> CURRENT FILING DATE: 2000-04-19  
 12 <150> PRIOR APPLICATION NUMBER: 60/130,403  
 13 <151> PRIOR FILING DATE: 1999-04-19  
 15 <160> NUMBER OF SEQ ID NOS: 4  
 17 <170> SOFTWARE: PatentIn Ver. 2.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 978  
 21 <212> TYPE: DNA  
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 31 1 5 10 15  
 33 cca tca tct ctc tca caa aag act cta ata tct tca cca aga ttc gtc 96  
 34 Pro Ser Ser Leu Ser Gln Lys Thr Leu Ile Ser Ser Pro Arg Phe Val  
 35 20 25 30  
 37 aat aac cct agc aga cgg agt cca ata cga tcc gtt ctt caa ttt aat 144  
 38 Asn Asn Pro Ser Arg Arg Ser Pro Ile Arg Ser Val Leu Gln Phe Asn  
 39 35 40 45  
 41 cgc aaa ccg gaa ctc gcc gga gaa acg ccg cgt atc gtc gtt atc acc 192  
 42 Arg Lys Pro Glu Leu Ala Gly Glu Thr Pro Arg Ile Val Val Ile Thr  
 43 50 55 60  
 45 tcc gga aaa ggc ggt gtt gga aag acg aca acc acc gca aat gtc ggt 240  
 46 Ser Gly Lys Gly Gly Val Gly Lys Thr Thr Thr Ala Asn Val Gly  
 47 65 70 75 80  
 49 ctc tct ctc gct cgt tac ggt ttc tca gtt gtc gcc att gac gcc gac 288  
 50 Leu Ser Leu Ala Arg Tyr Gly Phe Ser Val Val Ala Ile Asp Ala Asp  
 51 85 90 95  
 53 ctt ggt ctc cgt aac ctc gat ctc ctc cta ggg tta gag aat cga gtc 336  
 54 Leu Gly Leu Arg Asn Leu Asp Leu Leu Gly Leu Glu Asn Arg Val  
 55 100 105 110  
 57 aat tac act tgc gtc gag gtt ata aac gga gat tgt cgt ctc gat caa 384  
 58 Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln  
 59 115 120 125  
 61 gct ctg gta cgt gat aag cgt tgg tgg aat ttc gaa ttg cta tgt ata 432  
 62 Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile  
 63 130 135 140  
 65 tct aaa cct aga tgc aaa ctt ccg atg gga ttt ggt ggt aaa gca ttg 480  
 66 Ser Lys Pro Arg Ser Lys Leu Pro Met Gly Phe Gly Gly Lys Ala Leu  
 67 145 150 155 160

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69 gaa tgg ctt gtg gat gcg ttg aaa act aga ccg gaa ggt tca ccg gat 528
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73 ttc atc atc atc gat tgt cct gca gga atc gat gcc gga ttc ata acc 576
74 Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr
75      180      185      190
77 gcc att act ccg gcg aat gaa gca gtt ctg gta aca act ccg gat ata 624
78 Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile
79      195      200      205
81 aca gcg tta agg gat gct gat agg gtt acg ggt ttg tta gaa tgc gat 672
82 Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp
83      210      215      220
85 gga atc aga gat ata aag atg att gtg aac aga gtg aga act gat atg 720
86 Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Met
87 225      230      235      240
89 att aaa gga gag gat atg atg tca gtg tta gat gtg cag gag atg ttg 768
90 Ile Lys Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu
91      245      250      255
93 gga ttg tca ttg ctt ggt gta att cct gaa gat tct gag gtt att cga 816
94 Gly Leu Ser Leu Leu Gly Val Ile Pro Glu Asp Ser Glu Val Ile Arg
95      260      265      270
97 agc acg aat cga ggg ttt ccg ctt gtt ctg aat aag cct cct acg ctt 864
98 Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Thr Leu
99      275      280      285
101 gcg gga ttg gcg ttt gag cag gcg gct tgg aga ctc gtt gag caa gat 912
102 Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp
103      290      295      300
105 agt atg aag gct gtt atg gtg gag gaa gaa cct aag aaa cgt ggc ttc 960
106 Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly Phe
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110 Phe Ser Phe Phe Gly Gly
111      325
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124      20      25      30
126 Asn Asn Pro Ser Arg Arg Ser Pro Ile Arg Ser Val Leu Gln Phe Asn
127      35      40      45
129 Arg Lys Pro Glu Leu Ala Gly Glu Thr Pro Arg Ile Val Val Ile Thr
130      50      55      60
132 Ser Gly Lys Gly Gly Val Gly Lys Thr Thr Thr Ala Asn Val Gly
133      65      70      75      80
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Output Set: N:\CRF3\05042000\I553431.raw

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139          100          105          110
141 Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln
142          115          120          125
144 Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile
145          130          135          140
147 Ser Lys Pro Arg Ser Lys Leu Pro Met Gly Phe Gly Gly Lys Ala Leu
148 145          150          155          160
150 Glu Trp Leu Val Asp Ala Leu Lys Thr Arg Pro Glu Gly Ser Pro Asp
151          165          170          175
153 Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr
154          180          185          190
156 Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile
157          195          200          205
159 Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp
160          210          215          220
162 Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Met
163 225          230          235          240
165 Ile Lys Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu
166          245          250          255
168 Gly Leu Ser Leu Leu Gly Val Ile Pro Glu Asp Ser Glu Val Ile Arg
169          260          265          270
171 Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu
172          275          280          285
174 Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp
175          290          295          300
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188 <213> ORGANISM: Tagetes erecta
189 <220> FEATURE:
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192 <222> LOCATION: (50)..(934)
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197                               1
199 ctg agg ttt cta aca gaa ccc tca ctt gta tgc tca tcc act ttc ccc 106
200 Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser Thr Phe Pro
201          5          10          15
203 aca ttc aat ccc cta cac aaa acc cta act aaa cca aca cca aaa ccc 154
204 Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr Pro Lys Pro
205 20          25          30          35
207 tac cca aag cca cca cca att cgc tcc gtc ctt caa tac aat cgc aaa 202

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212 Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile Asp Ala Asp
213                               55                               60                               65
215 gtt ggt cta cgt aac ctc gat ctt ctt ctc ggt ctc gaa aac cgc gtc 298
216 Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val
217                               70                               75                               80
219 aat tac acc gtc gtt gaa gtt ctc aac ggc gat tgc aga ctc gac caa 346
220 Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg Leu Asp Gln
221                               85                               90                               95
223 gcc cta gtt cgt gat aaa cgc tgg tca aat ttc gaa ttg ctt tgt att 394
224 Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile
225 100                               105                               110                               115
227 tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga aaa gct tta 442
228 Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly Lys Ala Leu
229                               120                               125                               130
231 gtt tgg ctt gat gca tta aaa gat agg caa gaa ggt tgc ccg gat ttt 490
232 Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys Pro Asp Phe
233                               135                               140                               145
235 ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc ata acc gcc 538
236 Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr Ala
237                               150                               155                               160
239 att aca ccg gct aac gaa gcc gta tta gtt aca aca cct gat att act 586
240 Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile Thr
241                               165                               170                               175
243 gca ttg aga gat gca gat aga gtt aca ggc ttg ctt gaa tgt gat gga 634
244 Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp Gly
245 180                               185                               190                               195
247 att agg gat att aaa atg att gtg aac aga gtt aga act gat ttg ata 682
248 Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Leu Ile
249                               200                               205                               210
251 agg ggt gaa gat atg atg tca gtt ctt gat gtt caa gag atg ttg gga 730
252 Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu Gly
253                               215                               220                               225
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257                               230                               235                               240
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263 ttg gca ttt gag cag gct gct tgg aga ttg gtt gag caa gat agc atg 874
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267 aag gct gtg atg gtg gag gaa gaa cct aaa aag agg gga ttt ttc tcg 922
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269                               280                               285                               290
271 ttt ttt gga ggt tagtgcgaga attcggttgaa tcggttgagtt gggtttgttt 974
272 Phe Phe Gly Gly

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273          295
275 tgggtggagaa atgtgtcttg tttgttcacg taggagctgc tatgtgtcac ttgaaatggt 1034
277 atgtgtacag taagctgata aggattgttt taattcagtt ttcagagaga aaattagaat 1094
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285 <211> LENGTH: 295
286 <212> TYPE: PRT
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293 Thr Phe Pro Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr
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296 Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr
297 35 40 45
299 Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
300 50 55 60
302 Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Gly Leu Glu
303 65 70 75 80
305 Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg
306 85 90 95
308 Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu
309 100 105 110
311 Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly
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314 Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys
315 130 135 140
317 Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe
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320 Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro
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326 Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr
327 195 200 205
329 Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu
330 210 215 220
332 Met Leu Gly Leu Ser Leu Ser Asp Thr Arg Gly Phe Glu Val Ile
333 225 230 235 240
335 Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr
336 245 250 255
338 Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln
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344 Phe Phe Ser Phe Phe Gly Gly
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## VERIFICATION SUMMARY

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Input Set : A:\Un900411.app

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date